WHAT IS CLAIMED IS:

1.   A composition for preventing protein degradation, which contains an effective amount of small heat shock proteins (sHSPs).

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2.   The composition according to claim 1, wherein the sHSPs are one or more selected from proteins set forth in Table 1.

3.   The composition according to claim 2, wherein the sHSPs are one or more

10   selected from the group consisting of IbpA, IbpB, IbpAB and HSP26.

4.   A composition for use in 2-D gel electrophoresis, which contains an effective amount of sHSPs.

15   5.   The composition according to claim 4, wherein the sHSPs are one or more selected from the proteins set forth in Table 1.

6.   The composition according to claim 5, wherein the sHSPs are one or more selected from the group consisting of IbpA, IbpB, IbpAB and HSP26.

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7.   A method for the 2-D gel electrophoresis of a protein mixture, which comprising the steps of:
        adding sHSPs to the protein mixture, so as to prevent protein degradation and obtain gels with an increased number of spots; and

25   subjecting the protein mixture containing the sHSPs to 2-D gel electrophoresis.

8.   The method according to claim 7, wherein the sHSPs are one or more selected from the proteins set forth in Table 1.

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9.   The method according to claim 8, wherein the sHSPs are one or more selected from the group consisting of IbpA, IbpB and IbpAB derived from *E. coli*, IbpA derived from *Pseudomonas* and HSP26 derived from *Saccharomyces cerevisiae*.

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10.   The method according to claim 7, wherein the amount of the sHSPs that is added is in a range of 0.1 to 50 parts, relative to 100 parts by weight of the total protein of an electrophoresis sample.

10   11.   The method according to claim 10, wherein the amount of the sHSPs that is added is 0.5 to 20 parts, relative to 100 parts by weight of the total protein.

12.   The method according to claim 7, wherein the protein mixture is total protein in specific cells.

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13.   The method according to claim 12, wherein the specific cells are prokaryotes or eukaryotes.

14.   The method according to claim 13, wherein the prokaryotes are *E. coli* or

20   *Pseudomonas* sp. microorganisms, and the eukaryotes are human-derived cells.

15.   A method for the analysis of proteomes by 2-D gel electrophoresis, which is characterized by using the composition of claim 1.

25   16.   A method for using sHSPs as inhibitors of target protein degradation by protease.

17.   The method according to claim 16, wherein the sHSPs are one or more selected from proteins set forth in Table 1.

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